

RAW SEQUENCE LISTING

The Biotechnology Systems Branch of the Scientific and Technical Information Center (STIC) no errors detected.

Application Serial Number: 10/772,656A
Source: FW16
Date Processed by STIC: 7/31/07

ENTERED



IFW16

RAW SEQUENCE LISTING

DATE: 01/31/2007

PATENT APPLICATION: US/10/772,656A

TIME: 11:05:55

Input Set : N:\SSLM\10772656A.txt

Output Set: N:\CRF4\01302007\J772656A.raw

3 <110> APPLICANT: Saus, Juan
 4 Revert , Fernando
 5 Revert-Ros, Francisco
 7 <120> TITLE OF INVENTION: Novel Goodpasture antigen-binding protein isoforms and
 protein misfolded-
 8 mediated disorders
 10 <130> FILE REFERENCE: 03-075-US
 C--> 12 <140> CURRENT APPLICATION NUMBER: US/10/772,656A
 C--> 12 <141> CURRENT FILING DATE: 2004-02-05
 12 <150> PRIOR APPLICATION NUMBER: US 60/445,043
 13 <151> PRIOR FILING DATE: 2003-02-05
 15 <150> PRIOR APPLICATION NUMBER: US 60/445,003
 16 <151> PRIOR FILING DATE: 2003-02-05
 18 <150> PRIOR APPLICATION NUMBER: US 60/445,004
 19 <151> PRIOR FILING DATE: 2003-02-05
 21 <160> NUMBER OF SEQ ID NOS: 104
 23 <170> SOFTWARE: PatentIn version 3.1
 25 <210> SEQ ID NO: 1
 26 <211> LENGTH: 2389
 27 <212> TYPE: DNA
 28 <213> ORGANISM: Homo sapiens
 30 <220> FEATURE:
 31 <221> NAME/KEY: CDS
 32 <222> LOCATION: (409)..(2283)
 35 <400> SEQUENCE: 1
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 38 tctcttccct tcttttccct ttctcttccc tatttgaaat tggcatcgag ggggctaagt 120
 40 tcgggtggca gcgcggggcg caacgcaggg gtcacggcga cggcggcggc ggctgacggc 180
 42 tggaagggtta ggcttccttc accgctcgtc ctcttctctc gctccgctcg gtgtcaggcg 240
 44 cggcggcggc gcggcgggcg gacttcgtcc ctctctctgc tccccccac accggagcgg 300
 46 gcaactcttcg ctctgccatc ccccgacct tcaccccgag gactgggcgc ctctccggc 360
 48 gcagctgagg gagcgggggc cggctctctg ctcggttgtc gaggctcc atg tcg gat 417
 49 Met Ser Asp
 50 1
 52 aat cag agc tgg aac tcg tcg ggc tcg gag gag gat cca gag acg gag 465
 53 Asn Gln Ser Trp Asn Ser Ser Gly Ser Glu Glu Asp Pro Glu Thr Glu
 54 5 10 15
 56 tct ggg ccg cct gtg gag cgc tgc ggg gtc ctc agt aag tgg aca aac 513
 57 Ser Gly Pro Pro Val Glu Arg Cys Gly Val Leu Ser Lys Trp Thr Asn
 58 20 25 30 35
 60 tac att cat ggg tgg cag gat cgt tgg gta gtt ttg aaa aat aat gct 561
 61 Tyr Ile His Gly Trp Gln Asp Arg Trp Val Val Leu Lys Asn Asn Ala
 62 40 45 50
 64 ctg agt tac tac aaa tct gaa gat gaa aca gag tat ggc tgc aga gga 609

(Pg. 6)

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65	Leu	Ser	Tyr	Tyr	Lys	Ser	Glu	Asp	Glu	Thr	Glu	Tyr	Gly	Cys	Arg	Gly	
66				55					60					65			
68	tcc	atc	tgt	ctt	agc	aag	gct	gtc	atc	aca	cct	cac	gat	ttt	gat	gaa	657
69	Ser	Ile	Cys	Leu	Ser	Lys	Ala	Val	Ile	Thr	Pro	His	Asp	Phe	Asp	Glu	
70			70					75					80				
72	tgt	cga	ttt	gat	att	agt	gta	aat	gat	agt	gtt	tgg	tat	ctt	cgt	gct	705
73	Cys	Arg	Phe	Asp	Ile	Ser	Val	Asn	Asp	Ser	Val	Trp	Tyr	Leu	Arg	Ala	
74		85					90					95					
76	cag	gat	cca	gat	cat	aga	cag	caa	tgg	ata	gat	gcc	att	gaa	cag	cac	753
77	Gln	Asp	Pro	Asp	His	Arg	Gln	Gln	Trp	Ile	Asp	Ala	Ile	Glu	Gln	His	
78	100					105					110				115		
80	aag	act	gaa	tct	gga	tat	gga	tct	gaa	tcc	agc	ttg	cgt	cga	cat	ggc	801
81	Lys	Thr	Glu	Ser	Gly	Tyr	Gly	Ser	Glu	Ser	Ser	Leu	Arg	Arg	His	Gly	
82					120					125				130			
84	tca	atg	gtg	tcc	ctg	gtg	tct	gga	gca	agt	ggc	tac	tct	gca	aca	tcc	849
85	Ser	Met	Val	Ser	Leu	Val	Ser	Gly	Ala	Ser	Gly	Tyr	Ser	Ala	Thr	Ser	
86				135				140				145					
88	acc	tct	tca	ttc	aag	aaa	ggc	cac	agt	tta	cgt	gag	aag	ttg	gct	gaa	897
89	Thr	Ser	Ser	Phe	Lys	Lys	Gly	His	Ser	Leu	Arg	Glu	Lys	Leu	Ala	Glu	
90			150				155					160					
92	atg	gaa	aca	ttt	aga	gac	atc	tta	tgt	aga	caa	gtt	gac	acg	cta	cag	945
93	Met	Glu	Thr	Phe	Arg	Asp	Ile	Leu	Cys	Arg	Gln	Val	Asp	Thr	Leu	Gln	
94		165				170				175							
96	aag	tac	ttt	gat	gcc	tgt	gct	gat	gct	gtc	tct	aag	gat	gaa	ctt	caa	993
97	Lys	Tyr	Phe	Asp	Ala	Cys	Ala	Asp	Ala	Val	Ser	Lys	Asp	Glu	Leu	Gln	
98	180				185					190				195			
100	agg	gat	aaa	gtg	gta	gaa	gat	gat	gaa	gat	gac	ttt	cct	aca	acg	cgt	1041
101	Arg	Asp	Lys	Val	Val	Glu	Asp	Asp	Glu	Asp	Asp	Phe	Pro	Thr	Thr	Arg	
102				200						205				210			
104	tct	gat	ggg	gac	ttc	ttg	cat	agt	acc	aac	ggc	aat	aaa	gaa	aag	tta	1089
105	Ser	Asp	Gly	Asp	Phe	Leu	His	Ser	Thr	Asn	Gly	Asn	Lys	Glu	Lys	Leu	
106			215					220				225					
108	ttt	cca	cat	gtg	aca	cca	aaa	gga	att	aat	ggg	ata	gac	ttt	aaa	ggg	1137
109	Phe	Pro	His	Val	Thr	Pro	Lys	Gly	Ile	Asn	Gly	Ile	Asp	Phe	Lys	Gly	
110			230				235					240					
112	gaa	gcg	ata	act	ttt	aaa	gca	act	act	gct	gga	atc	ctt	gca	aca	ctt	1185
113	Glu	Ala	Ile	Thr	Phe	Lys	Ala	Thr	Thr	Ala	Gly	Ile	Leu	Ala	Thr	Leu	
114		245				250					255						
116	tct	cat	tgt	att	gaa	cta	atg	gtt	aaa	cgt	gag	gac	agc	tgg	cag	aag	1233
117	Ser	His	Cys	Ile	Glu	Leu	Met	Val	Lys	Arg	Glu	Asp	Ser	Trp	Gln	Lys	
118	260				265					270				275			
120	aga	ctg	gat	aag	gaa	act	gag	aag	aaa	aga	aga	aca	gag	gaa	gca	tat	1281
121	Arg	Leu	Asp	Lys	Glu	Thr	Glu	Lys	Lys	Arg	Arg	Thr	Glu	Glu	Ala	Tyr	
122				280					285					290			
124	aaa	aat	gca	atg	aca	gaa	ctt	aag	aaa	aaa	tcc	cac	ttt	gga	gga	cca	1329
125	Lys	Asn	Ala	Met	Thr	Glu	Leu	Lys	Lys	Lys	Ser	His	Phe	Gly	Gly	Pro	
126			295				300					305					
128	gat	tat	gaa	gaa	ggc	cct	aac	agt	ctg	att	aat	gaa	gaa	gag	ttc	ttt	1377
129	Asp	Tyr	Glu	Glu	Gly	Pro	Asn	Ser	Leu	Ile	Asn	Glu	Glu	Glu	Phe	Phe	

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130	310	315	320	
132	gat gct gtt gaa gct gct ctt gac aga caa gat aaa ata gaa gaa cag	1425		
133	Asp Ala Val Glu Ala Ala Leu Asp Arg Gln Asp Lys Ile Glu Glu Gln			
134	325 330 335			
136	tca cag agt gaa aag gtg aga tta cat tgg cct aca tcc ttg ccc tct	1473		
137	Ser Gln Ser Glu Lys Val Arg Leu His Trp Pro Thr Ser Leu Pro Ser			
138	340 345 350 355			
140	gga gat gcc ttt tct tct gtg ggg aca cat aga ttt gtc caa aag ccc	1521		
141	Gly Asp Ala Phe Ser Ser Val Gly Thr His Arg Phe Val Gln Lys Pro			
142	360 365 370			
144	tat agt cgc tct tcc tcc atg tct tcc att gat cta gtc agt gcc tct	1569		
145	Tyr Ser Arg Ser Ser Ser Met Ser Ser Ile Asp Leu Val Ser Ala Ser			
146	375 380 385			
148	gat gat gtt cac aga ttc agc tcc cag gtt gaa gag atg gtg cag aac	1617		
149	Asp Asp Val His Arg Phe Ser Ser Gln Val Glu Glu Met Val Gln Asn			
150	390 395 400			
152	cac atg act tac tca tta cag gat gta ggc gga gat gcc aat tgg cag	1665		
153	His Met Thr Tyr Ser Leu Gln Asp Val Gly Gly Asp Ala Asn Trp Gln			
154	405 410 415			
156	ttg gtt gta gaa gaa gga gaa atg aag gta tac aga aga gaa gta gaa	1713		
157	Leu Val Val Glu Glu Gly Glu Met Lys Val Tyr Arg Arg Glu Val Glu			
158	420 425 430 435			
160	gaa aat ggg att gtt ctg gat cct tta aaa gct acc cat gca gtt aaa	1761		
161	Glu Asn Gly Ile Val Leu Asp Pro Leu Lys Ala Thr His Ala Val Lys			
162	440 445 450			
164	ggc gtc aca gga cat gaa gtc tgc aat tat ttc tgg aat gtt gac gtt	1809		
165	Gly Val Thr Gly His Glu Val Cys Asn Tyr Phe Trp Asn Val Asp Val			
166	455 460 465			
168	cgc aat gac tgg gaa aca act ata gaa aac ttt cat gtg gtg gaa aca	1857		
169	Arg Asn Asp Trp Glu Thr Thr Ile Glu Asn Phe His Val Val Glu Thr			
170	470 475 480			
172	tta gct gat aat gca atc atc att tat caa aca cac aag agg gtg tgg	1905		
173	Leu Ala Asp Asn Ala Ile Ile Ile Tyr Gln Thr His Lys Arg Val Trp			
174	485 490 495			
176	cct gct tct cag cga gac gta tta tat ctt tct gtc att cga aag ata	1953		
177	Pro Ala Ser Gln Arg Asp Val Leu Tyr Leu Ser Val Ile Arg Lys Ile			
178	500 505 510 515			
180	cca gcc ttg act gaa aat gac cct gaa act tgg ata gtt tgt aat ttt	2001		
181	Pro Ala Leu Thr Glu Asn Asp Pro Glu Thr Trp Ile Val Cys Asn Phe			
182	520 525 530			
184	tct gtg gat cat gac agt gct cct cta aac aac cga tgt gtc cgt gcc	2049		
185	Ser Val Asp His Asp Ser Ala Pro Leu Asn Asn Arg Cys Val Arg Ala			
186	535 540 545			
188	aaa ata aat gtt gct atg att tgt caa acc ttg gta agc cca cca gag	2097		
189	Lys Ile Asn Val Ala Met Ile Cys Gln Thr Leu Val Ser Pro Pro Glu			
190	550 555 560			
192	gga aac cag gaa att agc agg gac aac att cta tgc aag att aca tat	2145		
193	Gly Asn Gln Glu Ile Ser Arg Asp Asn Ile Leu Cys Lys Ile Thr Tyr			
194	565 570 575			

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196 gta gct aat gtg aac cct gga gga tgg gca cca gcc tca gtg tta agg      2193
197 Val Ala Asn Val Asn Pro Gly Gly Trp Ala Pro Ala Ser Val Leu Arg
198 580                               585                               590                               595
200 gca gtg gca aag cga gag tat cct aaa ttt cta aaa cgt ttt act tct      2241
201 Ala Val Ala Lys Arg Glu Tyr Pro Lys Phe Leu Lys Arg Phe Thr Ser
202                               600                               605                               610
204 tac gtc caa gaa aaa act gca gga aag cct att ttg ttc tag              2283
205 Tyr Val Gln Glu Lys Thr Ala Gly Lys Pro Ile Leu Phe
206                               615                               620
208 tattaacagg tactagaaga tatgttttat ctttttttaa ctttatttga ctaatatgac    2343
210 tgtcaataact aaaatttagt tgttgaaagt atttactatg tttttt                2389
213 <210> SEQ ID NO: 2
214 <211> LENGTH: 624
215 <212> TYPE: PRT
216 <213> ORGANISM: Homo sapiens
218 <400> SEQUENCE: 2
220 Met Ser Asp Asn Gln Ser Trp Asn Ser Ser Gly Ser Glu Glu Asp Pro
221 1                               5                               10                               15
224 Glu Thr Glu Ser Gly Pro Pro Val Glu Arg Cys Gly Val Leu Ser Lys
225                               20                               25                               30
228 Trp Thr Asn Tyr Ile His Gly Trp Gln Asp Arg Trp Val Val Leu Lys
229                               35                               40                               45
232 Asn Asn Ala Leu Ser Tyr Tyr Lys Ser Glu Asp Glu Thr Glu Tyr Gly
233                               50                               55                               60
236 Cys Arg Gly Ser Ile Cys Leu Ser Lys Ala Val Ile Thr Pro His Asp
237 65                               70                               75                               80
240 Phe Asp Glu Cys Arg Phe Asp Ile Ser Val Asn Asp Ser Val Trp Tyr
241                               85                               90                               95
244 Leu Arg Ala Gln Asp Pro Asp His Arg Gln Gln Trp Ile Asp Ala Ile
245                               100                              105                              110
248 Glu Gln His Lys Thr Glu Ser Gly Tyr Gly Ser Glu Ser Ser Leu Arg
249                               115                              120                              125
252 Arg His Gly Ser Met Val Ser Leu Val Ser Gly Ala Ser Gly Tyr Ser
253                               130                              135                              140
256 Ala Thr Ser Thr Ser Ser Phe Lys Lys Gly His Ser Leu Arg Glu Lys
257 145                               150                               155                               160
260 Leu Ala Glu Met Glu Thr Phe Arg Asp Ile Leu Cys Arg Gln Val Asp
261                               165                               170                               175
264 Thr Leu Gln Lys Tyr Phe Asp Ala Cys Ala Asp Ala Val Ser Lys Asp
265                               180                               185                               190
268 Glu Leu Gln Arg Asp Lys Val Val Glu Asp Asp Glu Asp Asp Phe Pro
269                               195                               200                               205
272 Thr Thr Arg Ser Asp Gly Asp Phe Leu His Ser Thr Asn Gly Asn Lys
273                               210                               215                               220
276 Glu Lys Leu Phe Pro His Val Thr Pro Lys Gly Ile Asn Gly Ile Asp
277 225                               230                               235                               240
280 Phe Lys Gly Glu Ala Ile Thr Phe Lys Ala Thr Thr Ala Gly Ile Leu
281                               245                               250                               255
284 Ala Thr Leu Ser His Cys Ile Glu Leu Met Val Lys Arg Glu Asp Ser

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285          260          265          270
288 Trp Gln Lys Arg Leu Asp Lys Glu Thr Glu Lys Lys Arg Arg Thr Glu
289          275          280          285
292 Glu Ala Tyr Lys Asn Ala Met Thr Glu Leu Lys Lys Lys Ser His Phe
293          290          295          300
296 Gly Gly Pro Asp Tyr Glu Glu Gly Pro Asn Ser Leu Ile Asn Glu Glu
297 305          310          315          320
300 Glu Phe Phe Asp Ala Val Glu Ala Ala Leu Asp Arg Gln Asp Lys Ile
301          325          330          335
304 Glu Glu Gln Ser Gln Ser Glu Lys Val Arg Leu His Trp Pro Thr Ser
305          340          345          350
308 Leu Pro Ser Gly Asp Ala Phe Ser Ser Val Gly Thr His Arg Phe Val
309          355          360          365
312 Gln Lys Pro Tyr Ser Arg Ser Ser Ser Met Ser Ser Ile Asp Leu Val
313          370          375          380
316 Ser Ala Ser Asp Asp Val His Arg Phe Ser Ser Gln Val Glu Glu Met
317 385          390          395          400
320 Val Gln Asn His Met Thr Tyr Ser Leu Gln Asp Val Gly Gly Asp Ala
321          405          410          415
324 Asn Trp Gln Leu Val Val Glu Glu Gly Glu Met Lys Val Tyr Arg Arg
325          420          425          430
328 Glu Val Glu Glu Asn Gly Ile Val Leu Asp Pro Leu Lys Ala Thr His
329          435          440          445
332 Ala Val Lys Gly Val Thr Gly His Glu Val Cys Asn Tyr Phe Trp Asn
333          450          455          460
336 Val Asp Val Arg Asn Asp Trp Glu Thr Thr Ile Glu Asn Phe His Val
337 465          470          475          480
340 Val Glu Thr Leu Ala Asp Asn Ala Ile Ile Ile Tyr Gln Thr His Lys
341          485          490          495
344 Arg Val Trp Pro Ala Ser Gln Arg Asp Val Leu Tyr Leu Ser Val Ile
345          500          505          510
348 Arg Lys Ile Pro Ala Leu Thr Glu Asn Asp Pro Glu Thr Trp Ile Val
349          515          520          525
352 Cys Asn Phe Ser Val Asp His Asp Ser Ala Pro Leu Asn Asn Arg Cys
353          530          535          540
356 Val Arg Ala Lys Ile Asn Val Ala Met Ile Cys Gln Thr Leu Val Ser
357 545          550          555          560
360 Pro Pro Glu Gly Asn Gln Glu Ile Ser Arg Asp Asn Ile Leu Cys Lys
361          565          570          575
364 Ile Thr Tyr Val Ala Asn Val Asn Pro Gly Gly Trp Ala Pro Ala Ser
365          580          585          590
368 Val Leu Arg Ala Val Ala Lys Arg Glu Tyr Pro Lys Phe Leu Lys Arg
369          595          600          605
372 Phe Thr Ser Tyr Val Gln Glu Lys Thr Ala Gly Lys Pro Ile Leu Phe
373          610          615          620
376 <210> SEQ ID NO: 3
377 <211> LENGTH: 2311
378 <212> TYPE: DNA
379 <213> ORGANISM: Homo sapiens

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RAW SEQUENCE LISTING ERROR SUMMARY
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Please Note:

Use of n and/or Xaa have been detected in the Sequence Listing. Please review the Sequence Listing to ensure that a corresponding explanation is presented in the <220> to <223> fields of each sequence which presents at least one n or Xaa.

Seq#:104; Xaa Pos. 15 ✓

Invalid Line Length:

The rules require that a line not exceed 72 characters in length. This includes spaces.

Seq#:1; Line(s) 7 ✓

Invalid <213> Response:

Use of "Artificial" only as "<213> Organism" response is incomplete, per 1.823(b) of New Sequence Rules. Valid response is Artificial Sequence.

Seq#:9,10,11,12,13,14,15,16,17,18,19,20,21,22,23,24,25,26,27,28,29,30,31,32,33

Seq#:34,35,36,37,38,39,40,41,42,43,44,45,46,47,48,49,50,51,52,53,54,55,56,57

Seq#:58,59,60,61,62,63,64,65,66,67,68,69,70,71,72,73,74,75,76,77,78,79,80,81

Seq#:82,83,84,85,86,87,88,89,90,91,92,102,103,104

VERIFICATION SUMMARY

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L:12 M:270 C: Current Application Number differs, Replaced Current Application No

L:12 M:271 C: Current Filing Date differs, Replaced Current Filing Date

L:8200 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:104 after pos.:0